Mapreduce To Efficiently Extract Associations Between Biomedical Concepts From Large Text Data

V.Ramakrishna, Ch. Shravani

ABSTRACT--- Good sized biomedical content data is an crucial wellspring of facts that allows scientists to find top to bottom learning of organic frameworks, in addition to that well being experts can perform evidence primarily based prescription in a medical putting. be that as it could, the exam and investigation of those statistics is regularly the 2 statistics escalated and method concentrated. in this newsletter, we check out how map reduce, a parallel and appropriated programming worldview, may be applied to proficiently recognize the connections between biomedical thoughts got from an expansive range of biomedical articles. First of all, biomedical thoughts had been outstanding by using coordinating content material with the Unified Medical Language System (UMLS) Metathesaurus, a biomedical vocabulary and preferred database. We at that point built up a MapReduce calculation that may be applied to compute a class of intrigue measurements characterized primarily based on a 2 × 2 opportunity desk. This calculation accommodates of two Mapreduce employments and utilizations a stripe way to deal with diminish the quantity of center of the street outcomes. The examinations have been finished utilizing Amazon Elastic Mapreduce (EMR) with 33,960 articles from the TREC (Text Retrieval Conference) 2006 genomics tune. The execution test established that our calculation had roughly instantly adaptability and turned into more effective than a "matched" technique within the writing. The professional in our undertaking group analyzed a subset of the association debasement consequences identified with the remedy of drugs associated maladies and located that critical association regulations had been a high need.

Keywords: MapReduce High-Overall performance computing Association mining Biomedical literature.

1. INTRODUCTION

Biomedical analysts and social coverage providers distribute an intensive wide variety of clinical and studies articles every yr. a large element of those articles are reachable at the internet. they give an vital wellspring of data that not just permits specialists to pick out up pinnacle to bottom facts of natural frameworks, but in addition to assist human offerings experts utilize proof based totally prescription in clinical settings. [1,2]. inside the biomedical field, PubMed [3] is the most compelling on the internet database created and stored up through the national center for biotechnology records of the library of medication. PubMed carries in extra of 24 million references and continuously about 10.0 zero references are added to the database. Those articles have pulled in numerous scientists in information restoration and content mining [4]. Connection extraction is an imperative class for the disclosure of biomedical getting to know [5, 6], as locating the connections between biomedical thoughts or materials (Eg, features and maladies, meds and unfriendly occasions, and so on.) is often An problem key goal is for herbal and medicinal analysts. Exclusive approaches were utilized for biomedical courting extraction, for example, occasion insights [7], rule-based methodologies [8], layout mastering [9] and grouping [10-12]. As of past due, some examinations have endeavored to utilize affiliation mining strategies to discover biomedical connections in biomedical writing. As an example, Shetty et al. researched whether the usage of affiliation Mining on PubMed exposed imperative dating for unfriendly medicine events [13].

Xu et al. exhibited that medicate specific effect units were given from biomedical writing utilizing an assortment of methodologies, together with affiliation mining, could altogether decorate the discovery of post-promoting drug security signals [14]. Association mining means to find association leads as $X \rightarrow Y$, in which x and y are specific arrangements of additives, I. H. $X \cap Y = \emptyset$ [15]. An association determine suggests that the nearness of x shows the nearness of y. The utilization of affiliation mining methods to take away connections from biomedical writing is a test. From one angle, this is an statistics concentrated mission due to the sizeable extent of biomedical writing. Then again, that is moreover a computationally escalated task when you consider that the way toward setting apart biomedical thoughts, shaping all workable association governs and ascertaining the general exceptional of each affiliation rule depending on a particular intrigue measure, is extraordinarily tedious on the expansive range of biomedical thoughts. Mapreduce is a parallel and conveyed programming model for making ready quite a few facts in ware server businesses. As a pioneer in giving distributed computing administrations, Amazon gives an internet management called Amazon Elastic Map Reduce (EMR), which makes use of hadoop to address an Amazon-gave bunch of servers. With EMR and Amazon allotted computing engineering, it's something but difficult to begin a hadoop group with out agonizing over diffused factors, as an example, bunch setup, hadoop layout, and many others.

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V.Ramakrishna, Assistant Professor, Dept. Of Computer Science and Engineering, Anurag Group Of Institution Hyderabad. (E-mail: mekrikshnait2111@gmail.com)

Ch. Shravani, Post Graduate Student, Dept. Computer Science and Engineering , Anurag Group of Institutions, Hyderabad. (E-mail: chilukamarishravani25@gmail.com)

Clients can likewise adaptably pick the sort and variety of hubs and further the product units whilst beginning a group.

Paintings in this exam turned into directed on Amazon EMR. Using a partition and-vanquish approach, Map Reduce addresses expansive information issues in degrees: mapping and crumbling. In the manual degree, the information is separated into numerous parcels, which are treated autonomously of one another in parallel. Inside the decrease stage, the aftereffects of every section are joined to get the last outcomes or contribution for every other guide lower work. With this straightforward programming model, software program engineers can concentrate on top of the road facts getting ready methodologies, even as the Map Reduce gadget handles points of hobby of parallel execution. In mild of its straightforwardness, versatility, and variation to non-essential failure, Map Reduce has been utilized to manner large measures of statistics in one-of-a-kind fields [16-18]. Anyhow, there are simply a couple of concentrates at the usage of Map Reduce in biomedical association mining. Fan et al. utilized Map Reduce to discover manageable medicinal drug tranquilize communications with unfriendly remedy responses depending on auxiliary unconstrained FDA (meals and drug management) reports [19]. On this research we attempted to find out the connection between biomedically giant phrases from unfastened messages in biomedical writing. In this work, we received biomedical thoughts by means of adjusting content to traditional ideas characterised within the Unified Medical Language System (UMLS) [20, 21] Metathesaurus. We at that factor proposed a "stripe" manner to deal with compute the synchronous event of multiple thoughts within the card stage. this technique is greater gifted in light of the fact that it transmits fundamentally much less key-esteem sets than fan et al. likewise, our methodology requires just two MapReduce occupations to check in the closing estimations of an exciting activity for each affiliation rule, while fan's methodology calls for 3 MapReduce employments.

2. MAPREDUCE ALGORITHM DESIGN

There are two techniques to symbolize within the MapReduce programming model: Map () and Reduce (). The Map () method peruses a rundown of (key1, value1) units from the information records and computes any number of slight key esteem sets (key2, value2). In this examination, enter facts is an arrangement of news. Key1 indicates a document identity and value1 is the substance of the file. The middle of the road sets are assembled by using key and (key2, listing (value2)) is produced with the aid of the MapReduce system. In any case map errands are completed, the lessen () method is then connected to all characteristics (i.e., listing (value2)) associated with a comparable mild key to create yield key-esteem sets. at every degree, the shape designs appoint assignments or lower undertakings to diverse employees with the aim that they maintain going for walks in parallel. Discern 1 demonstrates the pseudo code of our map () strategy. To extra effectively make clear our calculation, allow us to assume that the data is an example informational index containing the 2 records d 1 and d 2. The Map Reduce structure guarantees that each document is handled by way of a mapper, a consultant allocated a guide undertaking. 2 indicates the information (i.e., the 2 data) and the yield of the technique. Table ii carries a rundown of the documentations applied in Fig. a letter portrays a biomedical idea in an archive. The request wherein the ideas are shown in a record is from left to proper. The info statistics shows that thoughts d and e display up twice in d 1 and d 2, for my part. Different ideas are proven as soon as in every record.

```
method MAP(docid id, doc d)
  A ← new ArrayList;
  for each concept c ∈ d
    if(A.contains(c) = false)
      A.add(c);
  end for
  SORT(A);
  for each concept c_i ∈ A, 1 ≤ i ≤ A.length()
    H ← new HashMap;
    H{c_i} ← 1;
    If(i ≠ A.length())
      for each concept c_j ∈ A, i < j ≤ A.length()
        H{c_i:c_j} ← 1;
      end for
    end if
    EMIT(concept c_i, hashmap H);
  end for
end method
```

Fig. 1. Pseudo-code for the Map ( ) approach.

input	*Mapper 1:*	A D B D (*document d1*)
	Mapper 2:	D E A E (*document d2*)
output	*Mapper 1:*	{A, [(A 1) (AB 1) (AD 1)]}
		{B, [(B 1) (BD 1)]}
		{D, [(D 1)]}
	Mapper 2:	{A, [(A 1) (AD 1) (AE 1)]}
		{D, [(D 1) (DE 1)]}
		{E, [(E 1)]}

Fig. 2. Input and output of the Map ( ) technique given the example dataset.

Table I: Example interestingness measures primarily based on 2 × 2 contingency table.

Measure	Definition
Correlation ($\emptyset$)	$(N f_{XY} - f_X f_Y)/\sqrt{f_X f_Y f_{\bar{X}} f_{\bar{Y}}}$
Cosine (IS)	$f_{XY}/\sqrt{f_X f_Y}$
Interest (I)	$N f_{XY}/f_X f_Y$
Jaccard (ζ)	$f_{XY}/(f_X + f_Y - f_{XY})$
Odds ratio (α)	$f_{XY} f_{\bar{X}\bar{Y}} / f_{\bar{X}Y} f_{X\bar{Y}}$
…	…

Table IIA list of notations used in Fig. 2.

Notation	Explanation
Letters A, B, ⋯	A letter represents a concept. It can also be used as the key of a key-value pair. Two letters together represent a concept pair. E.g., AB represents a pair (A, B).
Numbers 1, 2, ⋯	A number indicates the frequency count of a concept or concept pair.
{⋯, ⋯}	Represents a key-value pair.
[⋯]	Represents the value of a key-value pair.
(⋯)	Represents an entry of the value of a key-value pair.

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The primary circle (lines 3-6) in Map () peruses each idea in a record and produces a rundown of one in every of a kind ideas. That is, {A D B} and {D E A} are created for d 1 and d 2, individually. Line 7 kinds the rundown lexicographically. In this way, the two records are changed over to {A B D} and {A D E}. This progression guarantees that once two ideas are converged into the accompanying settled circle, the lower lexicographical request concept dependably is going earlier than the better request thoughts. This keeps a strategic distance from the probability of creating two specific units with a similar two ideas. With out the arranging undertaking, for example, d 1 could create an concept healthy {A, D} and d 2 {D, A}, which we don't need. The following settled circle (lines 8-17) produces each concept and its associated combines and yields the results. Given that we utilize a document with one event for each archive, the wide variety for every concept and every one in every of its associated sets is 1. in pseudocode, every concept is utilized as a hash key, and H {ci} is the hash an incentive for the hash. Key ci. We make use of a "strip" method. Every concept and its related units are put away in a hash delineate, and the complete H is viewed as an esteem this is yield alongside the idea that is the key. interestingly, fan et al. pick out an non-obligatory technique and straightforwardly communicated each idea and every co-occasion concept integrate to add.

Definitely, our method offers many less transitional units than the fan approach. For instance, if a record consists of m unique ideas, our methodology creates numerous O(m) sets, whilst the technique of fan o produces (m2) units. For the reason that midway yields produced via the map () technique are at the start organized domestically to acquire key-esteem units with a comparable key, the MapReduce execution device performs less kinds in our methodology and is on this way more powerful. The pseudocode of our lessen () strategy is seemed in parent three. This strategy executes a primary entirety of all the hash maps related with a comparable key. The MapReduce shape guarantees that each one hashaps with a comparable key are conveyed to a similar reducer for dealing with. given the example informational collection, data and yield of the Reduce() technique are given in FIG. because the informational series carries four one of a kind ideas (i.e., A, B, D, and E) and every idea is a key, the slight yields are separated into 4 gatherings and each gathering is dealt with by way of a reducer. The recurrence numbers associated with a similar idea or suit in numerous hash maps were cumulated and the results placed away in every reducer in some other hashmap. The last hashmap could be issued with a comparable key. At the yield of the reduce () approach, it creates the impression that the remaining mission handy is not adjusted between diverse reducers on the grounds that a few reducers (Eg reducer 1) must procedure a bigger variety of facts than others. In a real expansive scale utility, the amount of decrease assignments is normally loads greater noteworthy than the amount of reducers. this means every reducer frequently plays out numerous or maybe numerous errands at diverse events.

```
method REDUCE(concept c, hashmaps[H_1, H_2 ... H_m] )
  H <— new HashMap;
  for each hashmap H_i ∈ hashmaps[H_1, H_2 ... H_m]
    for each key k ∈ H_i
      if(H.contains(k))
        H{k} <— H{k} + H_i{k};
      else
        H.add(k, H_i{k});
    end for
  end for
  EMIT(concept c_i, hashmap H);
end method
```

Fig. 3. Pseudo-code for the Reduce ( ) method.

input	*Reducer 1:*	{A, [(A 1) (AB 1) (AD 1)] [(A 1) (AD 1) (AE 1)]}
	Reducer 2:	{B, [(B 1) (BD 1)]}
	Reducer 3:	{D, [(D 1)] [(D 1) (DE 1)]}
	Reducer 4:	{E, [(E 1)]}
output	*Reducer 1:*	{A, [(A 2) (AB 1) (AD 2) (AE 1)]}
	Reducer 2:	{B, [(B 1) (BD 1)]}
	Reducer 3:	{D, [(D 2) (DE 1)]}
	Reducer 4:	{E, [(E 1)]}

Fig. 4. Input and output of the Reduce ( ) method given the example dataset.

Further, the MapReduce framework makes use of a runtime scheduling scheme to run its map and reduce responsibilities. Accordingly, Greater assignments are handled at quicker hubs to guarantee stack adjusting. what is more, the Mapeduce scheduler utilizes a repetitive execution conspire. Inactive nodes execute the duties redundantly on rising nodes. The nodes that do their jobs earlier will output the consequences. After completing the above MapReduce activity, we nonetheless do no longer have sufficient data to calculate the interest metrics defined in table I. for each pair inside the very last hashmap generated by way of the Reduce() method, its frequency is thought. Similarly, the matter for the primary idea of the pair also can be retrieved from the same hashmap. This is, if a concept pair (X, Y), fXY and fX are regarded after the MapReduce activity. The subsequent step is the efficient calculation of f y given the output of the primary MapReduce task. As soon as fY is performed, the subsequent equations may be used to locate fXY, fXY and fXY:

$$f_{X\bar{Y}} = f_X - f_{XY} \quad \textbf{(1)}$$

$$f_{\bar{X}Y} = f_Y - f_{XY} \quad \textbf{(2)}$$

$$f_{\bar{X}\bar{Y}} = N - f_{XY} - f_{X\bar{Y}} - f_{\bar{X}Y} \quad \textbf{(3)}$$

In which N is the whole variety of files within the file. To calculate fY, we designed every other MapReduce activity. We use Map2() and Reduce2 () to render the map or reduce the methods within the 2nd MapReduce job. Figure 5 indicates the enter and output of the Map2() approach for the sample dataset.

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input	*Mapper 1:*	{A, [(A 2) (AB 1) (AD 2) (AE 1)]}
	Mapper 2:	{B, [(B 1) (BD 1)]}
	Mapper 3:	{D, [(D 2) (DE 1)]}
	Mapper 4:	{E, [(E 1)]}
output	*Mapper 1:*	{A, [(A 2)]} {B, [(AB 1 2)]}{D, [(AD 2 2)]} {E, [(AE 1 2)]}
	Mapper 2:	{B, [(B 1)]} {D, [(BD 1 1)]}
	Mapper 3:	{D, [(D 2)]} {E, [(DE 1 2)]}
	Mapper 4:	{E, [(E 1)]}

Fig. 5. Input and output of the Map2( ) method approach given the instance dataset.

input	*Reducer 1:*	{A, [(A 2)]}
	Reducer 2:	{B, [(B 1) (AB 1 2)]}
	Reducer 3:	{D, [(D 2) (AD 2 2) (BD 1 1)]}
	Reducer 4:	{E, [(E 1) (AE 1 2) (DE 1 2)]}
output	*Reducer 1:*	None
	Reducer 2:	{AB, [(V_{AB})]}
	Reducer 3:	{AD, [(V_{AD})]} {BD, [(V_{BD})]}
	Reducer 4:	{AE, [(V_{AE})]} {DE, [(V_{DE})]}

Fig. 6. Input and output of the Reduce2( ) approach given the instance dataset.

The contribution of the Map2( ) strategy is the final hashmap transmitted via the Reduce( ) approach from the final MapReduce work. The Map2( ) approach peruses the substance of the hashmap and first transmits the unmarried concept and its tally from the hashmap. For instance, X, {X *f* X } is emitted for idea X. This is, if X = A and *f*X =2, then A , [A 2] is emitted (see Fig5). Concept X is moreover the main idea of each healthy in the hashmap. The method at that factor provides the tally of the single concept to each match passage inside the hashmap. After that, each new pair entry is emitted the use of the second concept of the pair as the key. this is, for an access (XYf_{XY}), Y , [(XY$f_{XY}f_X$)] is emit- ted. Inside the reduce segment, each reducer receives fY and the informa- tion of all pairs whose second idea is Y considering the fact that they have the equal key. As fX is already connected to a concept pair (X, Y), the reducer has all the 3 values fXY ,fX, and fY. With those values, fXY, fXY and fXY can be computed the use of Eqs (1)-(three). The reducer currently has sufficient records to discern the estimation of any intriguing quality degree in Table I. We utilize VXY to talk to the estimation of an intriguing first-class degree for the fit. This esteem is produced by means of the reducer with the combine as the important thing. The enter and output of the Reduce2( ) approach is given in Fig.6. Notice that Reduce1 has no output when you consider that Its enter does not encompass any pairs. For actual applications with hundreds or even millions of concepts, every reducer is assigned to procedure the input information associated with many keys.

Alongside those lines, every reducer frequently figures the estimation of the intrigue ingness degree for loads of sets. As the pseudo codes for Map2( ) and Reduce2( ) are clear, they are no longer given in the content. We officially depicted one favorable role of the stripes technique – it emanates many much less key-esteem units in view that all idea units beginning with a similar idea are bundled into one hashmap. Any other favored perspective of this methodology is that only a unmarried greater MapReduce work is must get the closing results; each fXY and fX are received for an concept combine (x, y) after the first MapReduce paintings. On the off danger that fan's technique changed into utilized (i.e., every suit is discharged independently), extra MapReduce occupations may be required – one employment is utilized to get fX ,whilst the alternative one is utilized to get fY.

3. RESULT

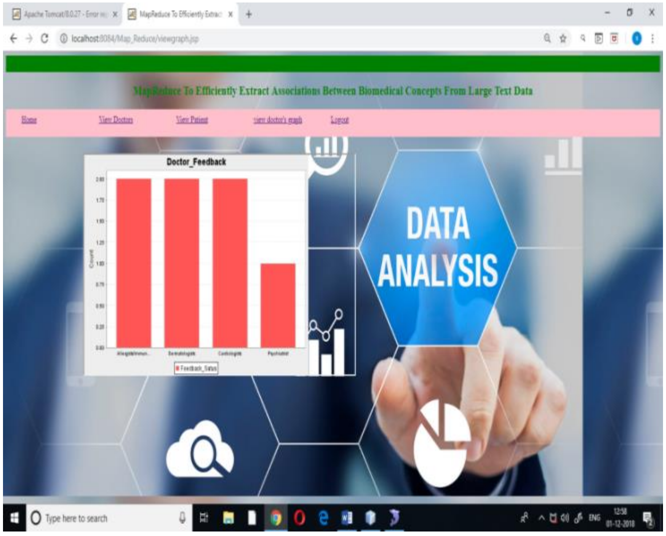

Fig 2. View Doctors Graph

4. CONCLUSION

We've built up an powerful MapReduce calculation to com-pute the nice of relationship between any biomedical con-cepts that display up in an arrangement of biomedical records. This calculation can be connected to any fascinating excellent degree that relies upon on a 2 ×2 opportunity table. Biomedical ideas were gotten by coordinating every expression in an archive to UMLs metathesaurus. We contrasted our technique and a sets method using 33,960 complete-content material articles from TREC 2006 genomics tune on Amazon's EMR stage. The consequences showed that our methodology became extensively extra productive. We likewise explored the versatility of our calculation. The consequences proven that, while our calculation's versatility changed into approx-imately directly concerning the number hubs within the organization, it changed into a ways and away superior to direct adaptability as some distance as records degree. Likewise, a subset of affiliation regulations identified with medicinal drug sickness deal with-ment become explored by means of the health practitioner in our exploration collecting. the assessment results confirmed that giant affiliation rules have been found to be located high.

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